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RAW SEQUENCE LISTING DATE: 01/29/2001
PATENT APPLICATION: US/09/759,207 TIME: 13:14:20

Input Set : A:\Seq.txt
Output Set: N:\CRF3\01292001\I759207.raw

SEQUENCE LISTING

- 3 (1) GENERAL INFORMATION:

4 (i) APPLICANT: Iris Pecker et al.

5 (ii) TITLE OF INVENTION: HEPARANASE SPECIFIC MOLECULAR PROBES
6 AND THEIR USE IN RESEARCH AND MEDICAL
7 APPLICATIONS

8 (iii) NUMBER OF SEQUENCES: 7

9 (iv) CORRESPONDENCE ADDRESS:

10 (A) ADDRESSEE: G. E. Ehrlich (1995) Ltd.
11 c/o Anthony Castorina

12 (B) STREET: 2001 Jefferson Davis Highway, Suite 207

13 (C) CITY: Arlington

14 (D) STATE: Virginia

15 (E) COUNTRY: United States of America

16 (F) ZIP: 22202

17 (v) COMPUTER READABLE FORM:

18 (A) MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk

19 (B) COMPUTER: Twinhead* Slimnote-890TX

20 (C) OPERATING SYSTEM: MS DOS version 6.2,
21 Windows version 3.11

22 (D) SOFTWARE: Word for Windows version 2.0 converted to
23 an ASCII file

24 (vi) CURRENT APPLICATION DATA:

25 (A) APPLICATION NUMBER: US/09/759,207

26 (B) FILING DATE: 16-Jan-2001

27 (C) CLASSIFICATION:

28 (vii) PRIOR APPLICATION DATA:

29 (A) APPLICATION NUMBER: 08/922,180

30 (B) FILING DATE: September 2, 1997

31 (A) APPLICATION NUMBER: 09/071,739

32 (B) FILING DATE: May 1, 1998

33 (A) APPLICATION NUMBER: 09/322,977

34 (B) FILING DATE: June 1, 1999

35 (viii) ATTORNEY/AGENT INFORMATION:

36 (A) NAME: Sol Sheinbein

37 (B) REGISTRATION NUMBER: 25,457

38 (C) REFERENCE/DOCKET NUMBER: 00/21505

39 (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: 972-3-6127676

41 (B) TELEFAX: 972-3-6127575

42 (C) TELEX:

44 (2) INFORMATION FOR SEQ ID NO: 1:

45 (i) SEQUENCE CHARACTERISTICS:

46 (A) LENGTH: 1721

47 (B) TYPE: nucleic acid

48 (C) STRANDEDNESS: double

49 (D) TOPOLOGY: linear

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C--> 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 51 CTAGACCTTT CGACTCTCCG CTCCGCCGCA GCTGCCGGC GGAGCACCCA CGTGACCCCA 60
 52 AGATGCTGCT GCCTCGAAG CCTGCCGCTGC CGCCGCCGCT GATGCTGCTG CTCCCTGGGC 120
 53 CGC'GGGTCC CCTC'CCCCT GGCGCCC'TGC CCCGACCTGC GCAAGCACAG GACGTCGTGC 180
 C--> 54 ACCTGGACTT CTTCACCCAG GAGCCGCTGC ACCTGGTGAG CCCCTCGTTC CTGTCGTCA 240
 55 CCATTGACCC CAACCTGGCC ACCGACCCCG CGTTCCTCAT CCTCCCTGGGT TCTCCAAACC 300
 56 TTGCGTACCTT GGCGAGAGGCTTGTCTCCGTG CGTACCTGAG GTTGGGTCGC ACCAACAGACAG 360
 57 ACTTCCTAAAT TTTCGATCCC AAGAAGGAAT CAAACCTTGAG AGAGAGAAAGT TACTGGCAAT 420
 58 CTCAAGTCAA CCACGATATT TGCAAAATATG GATCCATCCC TCCTGATGTG GAGCAGAAGT 480
 59 TACGGTTGGA ATGGCCCTAC CAGGAGCAAT TGCTACTCCG AGAACACTAC CAGAAAAAGT 540
 60 TCAAGAACAG CACCTACTCA AGAACGCTCG TAGATGTGCT ATACACTTTT GCAAACGTGCT 600
 61 CAGGACTGGA CTTGATCTT GGCCATAATG CGTATTAAAG AACAGCAGAT TTCCAGTGGA 660
 62 ACAGTTCTAA TGCTCAGTTG CTCCCTGGACT ACTGCTCTTC CAAGGGGTAT AACATTTCTT 720
 63 GGGAAACTAGG CAATGACCAAT AACAGTTTC TTAAGAAGGC TGATATTTCG ATCAATGGGT 780
 64 CGCAGTTAGG AGAAAGATTAT ATTCAATTGCA ATAACCTTCT AAAGAAAGTCC ACCTTCAAA 840
 65 ATGCAAAACT CTATGGCTCT GATGTTGGTC AGCCTCGAAG AAAGACGGCT AAGATGCTGA 900
 66 AGAGCTTCTT GAAGGCTGGT GGAGAAGTGA TTGATTCAGT TACATGGCAT CACTACTATT 960
 67 TGAATGGACG GACTGCTACC AGGGAAGATT TTCTAAACCC TGATGTATTG GACATTTTTA 1020
 68 TTTCATCTGT GCAAAAGTT TTCCAGGTGG TTGAGAGCAC CAGGCCTGGC AAGAAGGTCT 1080
 69 GGTTAGGAGA AACAAAGCTCT GCATATGGAG GCGGAGCGCC CTTGCTATCC GACACCTTTC 1140
 70 CAGCTGGCTT TATGTGGCTG GATAAATTGG GCCTGTCAGC CCGAATGGGA ATAGAAGTGG 1200
 71 TGATGAGGCA AGTATTCTTT GGAGCAGGAA ACTACCATTG AGTGGATGAA AACTTCGATC 1260
 72 CTTTACCTGA TTATTGGCTA TCTCTTCTGT TCAAGAAATTG GTGGGGCACC AAGGTGTTAA 1320
 73 TGGCAAGCGT GCAAGGCTCA AAGAGAAGGA AGCTCGAGT ATACCTTCAT TGCACAAACA 1380
 74 CTGACAATTC AAGGTATAAA GAAGGAGATT TAACCTGTG TGCCATAAAC CTCCATAACG 1440
 75 TCACCAAGTA CTTGCGGTTA CCCTATCCTT TTCTTAACAA GCAAGTGGAT AAATACCTTC 1500
 76 TAAGACCTTT GGGACCTCAT GGATTACTTT CCAAATCTGT CCAAACCTCAAT GGTCTAACTC 1560
 77 TAAAGATGGT GGATGATCAA ACCTTGCCAC CTTTAATGGG AAAACCTCTC CGGCCAGGAA 1620
 78 GTTCACTGGG CTTGCCAGCT TTCTCATATA GTTTTTCTG GATAAGAAAT GCCAAAGTTG 1680
 79 CTGCTTGCAAT CTGAAATAA AATATACTAG TCCTGACACT G 1721
 81 (2) INFORMATION FOR SEQ ID NO: 2:
 82 (i) SEQUENCE CHARACTERISTICS:
 83 (A) LENGTH: 543
 84 (B) TYPE: amino acid
 85 (C) STRANDEDNESS: single
 86 (D) TOPOLOGY: linear
 C--> 87 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 88 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
 89 5 10 15
 90 Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
 91 20 25 30
 92 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln-Glu Pro
 93 35 40 45
 94 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
 95 50 55 60
 96 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
 97 65 70 75 80
 98 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
 99 85 90 95

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107 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Glu Ser Thr Phe
108          100           105           110
110 Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
111          115           120           125
113 Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
114          130           135           140
116 Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
117 145          150           155           160
119 Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Val Leu Tyr Thr Phe
120          165           170           175
122 Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
123          180           185           190
125 Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
126          195           200           205
128 Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
129          210           215           220
131 Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
132 225          230           235           240
134 Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
135          245           250           255
137 Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
138          260           265           270
140 Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
141          275           280           285
143 Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
144          290           295           300
146 Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
147 305          310           315           320
149 Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
150          325           330           335
152 Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala
153          340           345           350
155 Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
156          355           360           365
158 Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
159          370           375           380
161 Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
162 385          390           395           400
164 Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
165          405           410           415
167 Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
168          420           425           430
170 Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
171          435           440           445
173 Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
174          450           455           460
176 Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
177 465          470           475           480
179 Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn

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180	485	490	495
182 Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met			
183	500	505	510
185 Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser			
186	515	520	525
188 Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile			
189	530	535	540 543
191 (2) INFORMATION FOR SEQ ID NO: 3:			
192 (i) SEQUENCE CHARACTERISTICS:			
193 (A) LENGTH: 1721			
194 (B) TYPE: Nucleic acid			
195 (C) STRANDEDNESS: Double			
196 (D) TOPOLOGY: linear			
C--> 197 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:			
199	CT AGA GCT TTC GAC	14	
201 TCT CCG CTG CGC GGC AGC TGG CGG GGG GAG CAG CCA GGT GAG CCC AAG	62		
203 ATG CTG CTG CGC TCG AAG CCT CCG CTG CCG CCG CTG ATG CTG CTG	110		
204 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu			
205	5 10	15	
207 CTC CTG GGG CCG CTG GGT CCC CTC TCC CCT GGC GCC CTG CCC CGA CCT	158		
208 Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro			
209	20 25	30	
211 GCG CAA GCA CAG GAC GTC GTG GAC CTG GAC TTC ACC CAG GAG CCG	206		
212 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro			
213	35 40	45	
215 CTG CAC CTG GTG AGC CCC TCG TTC CTG TCC GTC ACC ATT GAC GCC AAC	254		
216 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn			
217	50 55	60	
219 CTG GCC ACG GAC CCG CGG TTC CTC ATC CTC CTG GGT TCT CCA AAG CTT	302		
220 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu			
221	65 70	75 80	
223 CGT ACC TTG GCC AGA GGC TTG TCT CCT GCG TAC CTG AGG TTT GGT GGC	350		
224 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly			
225	85 90	95	
227 ACC AAG ACA GAC TTC CTA ATT TTC GAT CCC AAG AAG GAA TCA ACC TTT	398		
228 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe			
229	100 105	110	
231 GAA GAG AGA AGT TAC TGG CAA TCT CAA GTC AAC CAG GAT ATT TGC AAA	446		
232 Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys			
233	115 120	125	
235 TAT GGA TCC ATC CCT CCT GAT GTG GAG GAG TTA CGG TTG GAA TGG	494		
236 Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp			
237	130 135	140	
239 CCC TAC CAG GAG CAA TTG CTA CTC CGA GAA CAC TAC CAG AAA AAG TTC	542		
240 Pro Tyr Gln Glu Gln Leu Leu Arg Glu His Tyr Gln Lys Lys Phe			
241	145 150	155 160	
243 AAG AAC AGC ACC TAC TCA AGA AGC TCT GTA GAT GTG CTA TAC ACT TTT	590		
244 Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe			
245	165 170	175	

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PATENT APPLICATION: US/09/759,207

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247 GCA AAC TGC TCA GGA CTG GAC TTG ATC TTT GGC CTA AAT GCG TTA TTA 638
 248 Ala Asn Cys Ser Gly Leu Asp Ile Phe Gly Leu Asn Ala Leu Leu
 249 180 185 190
 251 AGA ACA GCA GAT TTG CAG TGG AAC ACT TCT AAT GCT CAG TTG CTC CTG 686
 252 Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
 253 195 200 205
 255 GAC TAC TGC TCT TCC AAG GGG TAT AAC ATT TCT TTG GAA CTA GGC AAT 734
 256 Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
 257 210 215 220
 259 GAA CCT AAC AGT TTC CTT AAG AAG GCT GAT ATT TTC ATC AAT GGG TCG 782
 260 Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
 261 225 230 235 240
 263 CAG TTA GGA GAA GAT TAT ATT CAA TTG CAT AAA CTT CTA AGA AAG TCC 830
 264 Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
 265 245 250 255
 267 ACC TTC AAA AAT GCA AAA CTC TAT GGT CCT GAT GTT GGT CAG CCT CGA 878
 268 Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
 269 260 265 270
 271 AGA AAG ACG GCT AAG ATG CTG AAG AGC TTC CTG AAG GCT GGT GGA GAA 926
 272 Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
 273 275 280 285
 275 GTG ATT GAT TCA GTT ACA TGG CAT CAC TAC TAT TTG AAT GGA CGG ACT 974
 276 Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
 277 290 295 300
 279 GCT ACC AGG GAA GAT TTT CTA AAC CCT GAT GTA TTG GAC ATT TTT ATT 1022
 280 Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
 281 305 310 315 320
 283 TCA TCT GTG CAA AAA GTT TTC CAG GTG GTT GAG AGC ACC AGG CCT GGC 1070
 284 Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
 285 325 330 335
 287 AAG AAG GTC TGG TTA GGA GAA ACA AGC TCT GCA TAT GGA GGC GGA GCG 1118
 288 Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Ala
 289 340 345 350
 291 CCC TTG CTA TCC GAC ACC TTT GCA GCT GGC TTT ATG TGG CTG GAT AAA 1166
 292 Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
 293 355 360 365
 295 TTG GGC CTG TCA GCC CGA ATG GGA ATA GAA GTG GTG ATG AGG CAA GTA 1214
 296 Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
 297 370 375 380
 299 TTC TTT GGA GCA GGA AAC TAC CAT TTA GTG GAT GAA AAC TTC GAT CCT 1262
 300 Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
 301 385 390 395 400
 303 TTA CCT GAT TAT TTG CTA TCT CTT CTG TTC AAG AAA TTG GTG GGC ACC 1310
 304 Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
 305 405 410 415
 307 AAG GTG TTA ATG GCA AGC GTG CAA GGT TCA AAG AGA AGG AAG CCT CGA 1358
 308 Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
 309 420 425 430
 311 GTA TAC CCT CAT TGC ACA AAC ACT GAC AAT CCA AGG TAT AAA GAA GGA 1406

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/759,207

DATE: 01/29/2001
TIME: 13:14:21

Input Set : A:\Seq.txt
Output Set: N:\CRF3\01292001\I759207.raw

L:4 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:25 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:26 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:50 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:54 M:111 C: (47) String data converted to upper case,
L:87 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:197 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:347 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:356 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:365 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:374 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]